

Evolution of metabolic diversity in polyketide-derived pyrones: using the non-colinear aureothin assembly line as a model system.

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Abstract

Polyketide-derived pyrones are structurally diverse secondary metabolites that are represented in all three kingdoms of life and are endowed with various biological functions. The aureothin family of *Streptomyces* metabolites was chosen as a model to study the factors governing structural diversity and the evolutionary processes involved. This review highlights recent insights into the non-colinear aureothin and neo-aureothin modular type I polyketide synthase (PKS), aromatic starter unit biosynthesis, polyketide tailoring reactions, and a non-enzymatic polyene splicing cascade. Pyrone biosynthesis in bacteria, fungi, and plants is compared. Finally, various strategies to increase metabolic diversity of aureothin derivatives through mutasynthesis, pathway engineering, and biotransformation are presented. The unusual aureothin and neo-aureothin assembly lines thus not only represent a model for PKS evolution, but provided important insights into non-canonical enzymatic processes that could be employed for the production of antitumor and antifungal agents.

Beteiligte Forschungseinheiten

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